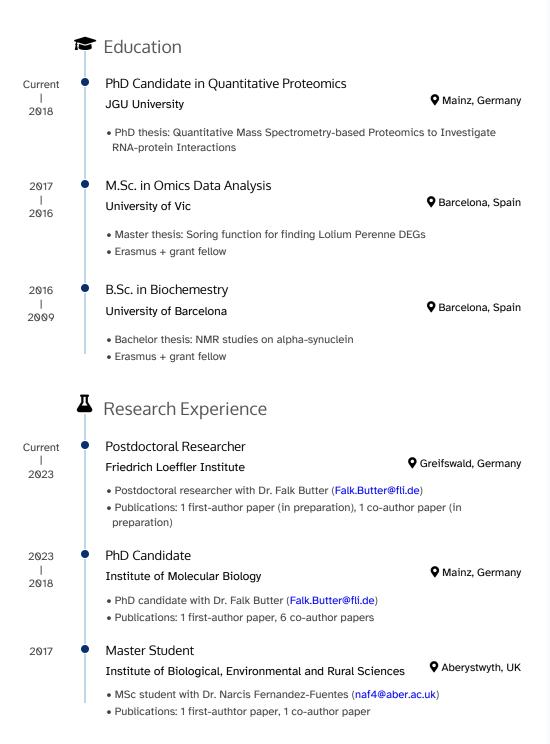# Albert Fradera Sola

Bioinformatician | Data Scientist | Proteomics & Genomics Scientist

I consider myself both collaborative and adaptable. I am always eager to take on new and diverse projects. I am very enthusiastic about sharing and continuously developing my data visualization skills as a means to enhance scientific communication. I am an open-minded person and enjoy fostering strong relationships with my colleagues.

🎓 Education

Current | 2018

PhD Candidate in Quantitative Proteomics
JGU University

📍 Mainz, Germany

- PhD thesis: Quantitative Mass Spectrometry-based Proteomics to Investigate RNA-protein Interactions

2017 | 2016

M.Sc. in Omics Data Analysis
University of Vic

📍 Barcelona, Spain

- Master thesis: Soring function for finding Lolium Perenne DEGs
- Erasmus + grant fellow

2016 | 2009

B.Sc. in Biochemestry
University of Barcelona

📍 Barcelona, Spain

- Bachelor thesis: NMR studies on alpha-synuclein
- Erasmus + grant fellow

🧪 Research Experience

Current | 2023

Postdoctoral Researcher
Friedrich Loeffler Institute

📍 Greifswald, Germany

- Postdoctoral researcher with Dr. Falk Butter (Falk.Butter@fli.de)
- Publications: 1 first-author paper (in preparation), 1 co-author paper (in preparation)

2023 | 2018

PhD Candidate
Institute of Molecular Biology

📍 Mainz, Germany

- PhD candidate with Dr. Falk Butter (Falk.Butter@fli.de)
- Publications: 1 first-author paper, 6 co-author papers

2017

Master Student
Institute of Biological, Environmental and Rural Sciences

📍 Aberystwyth, UK

- MSc student with Dr. Narcis Fernandez-Fuentes (naf4@aber.ac.uk)
- Publications: 1 first-authtor paper, 1 co-author paper

Contact

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Language Skills

Catalan	
Spanish	
English	
German	

My CV as a network

Bullet points (for 🎓, 🧪, 📧, and 👥) are interconnected by year. Interactive version here

🖥️ Dry Lab Projects and Related Skills

Network-based Assignment of RNA-Binding Proteins' Functionality

- Functionality was inferred from associations with annotations at the domain, molecular function, and pathway levels.
- Function-based networks were created from quantitative proteomics data and made accessible through an interactive, user-friendly web interface.
- **Keywords:** Network | Functional analysis | Pfam | GO | KEGG | R Shiny

Infectome Profiling of Three *Leishmania* Species

- *M. musculus* proteome changes were investigated after infection with *Leishmania*.
- Protein orthologs between the *Leishmania* species were established.
- **Keywords:** Proteome | Differential expression | Protein orthology

Embryonic Development Proteome Profiling of *Xenopus* Species

- Clustering (Self Organizing Maps) and dimensionality reduction techniques (Principal Component Analysis) were applied.
- **Keywords:** Proteome | Differential expression | SOM | PCA | Clustering

Scoring Function for RNA-Seq Differential Expression Assessment

- A scoring function was developed around three RNA-Seq differential expression assessment R packages (DESeq2, edgeR, limma+voom)
- **Keywords:** NGS | RNA-Seq | Quality control | Differential expression

ChIP-Seq Characterization of a Novel ATPase in *T. brucei*

- H2A.Z deposition was investigated and visualized with genome tracks
- **Keywords:** NGS | ChIP-Seq | Genome tracks

✏️ Wet Lab Projects and Related Skills

Immunoprecipitation of RNA-binding Proteins in *S. cerevisiae*

- I was responsible for designing the experimental setup and generating the data for the RNA-binding protein interactome investigation.
- **Keywords:** Yeast | Protein Immunoprecipitation | Experimental design

Mass Spectrometry Quantitative Proteomics

- I used chemical labeling (DML) and label-free mass spectrometry sample preparation protocols on several projects
- **Keyword:** Mass spectrometry | DML | LFQ | In-gel digestion

Coding Skills

- R
- Bash
- markdown
- css
- Python
- html

Some R packages I have experience with:

tidyverse | tidyr | dplyr
ggplot2 | Shiny | rmarkdown
DESeq2 | limma | edgeR
IRanges | Genomic Ranges | clusterProfiler
AnnotationDbi | biomaRt | ChIPseeker

Proteomics Software Skills

- MaxQuant
- Proteinortho
- InterPro

Genomics Software Skills

- STAR
- Bowtie
- FastQC
- MultiQC
- fastqscreen
- deepTools
- HTSeq
- MACS2
- rMATS

📖 Publications

Articles with Genomics Analysis

- 2022 | PLoS Pathogens | https://doi.org/10.1371/journal.ppat.1010514
- 2021 | Nature Comunications | https://doi.org/10.1038/s41467-021-22861-2
- 2021 | PLoS One | https://doi.org/10.1371/journal.pone.0249636
- 2019 | PLoS One | https://doi.org/10.1371/journal.pone.0220518

Articles with Proteomics Analysis

- 2023 | Nucleic Acid Research | https://doi.org/10.1093/nar/gkad245
- 2023 | iScience | https://doi.org/10.1016/j.isci.2023.106778
- 2023 | PLoS Pathogens | https://doi.org/10.1371/journal.ppat.1011486
- 2021 | Journal of Cell Science | https://doi.org/10.1242/jcs.254300
- 2020 | RNA | https://doi.org/10.1261/rna.076281.120

🖥 Conferences and Courses

Conferences

- 2022 | Statistical data analysis for genome-scale biology | Flash talk
- 2021 | Network biology | Plenary talk
- 2019 | FEBS advanced course | Poster presentation

Courses

- 2022 | Data visualization for scientists
- 2021 | Scientific writing
- 2020 | Convincing scientific presentations
- 2020 | Regression Models | Coursera certificate
- 2020 | Statistical Inference | Coursera certificate

Abstract word cloud

Abstracts from the publications are summarized into a word cloud.

Document created with the R packages pagedown and datadrivencv.

The source code is available on github.

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